Supplementary

Table S1 The final cutoff of high expression levels for each biomarker. When we calculated the effect of a biomarker, we analyzed the effects of different high-expression cutoff points (>0, >1, >2, and >3). When the effects of the biomarker expression levels were most significant, the cutoff of the expression level was determined to be the final cutoff point

Biomarker	Number of patients per score					Standard of high expression levels	Estimated effects (High *vs.* low, mm/year ± SE)	P-value
	0	1	2	3	4			
ATRX	9	9	3	1	3	>0	-2.5±0.4	0.16×10^{-8}*
						>1	-2.3±0.4	0.68×10^{-7}
						>2	-1.2±1.2	0.34
						>3	-1.9±1.3	0.16
EGFR	0	0	4	3	9	>0	-	
						>1	-	
						>2	1.0±0.9	0.27
						>3	1.8±0.6	0.003*
Mutant p53	9	7	6	3	5	>0	-0.7±0.7	0.28
						>1	2.4±0.4	0.14×10^{-8}
						>2	3.0±0.4	0.12×10^{-10}*
						>3	2.6±0.5	0.4×10^{-6}
Ki-67	0	18	15	1	2	>0	-	-
						>1	-0.7±0.4	0.05*
						>2	1.7±0.9	0.07
						>3	1.6±1.0	0.10

*, A P-value ≤0.05 was considered statistically significant. SE, standard error.

Table S2 Comparing the VDE between 2 subgroups (complete or missing molecular data) to assess potential bias from missing data

Molecular biomarker	Number of patients in subgroup		eVDE (mm/year)	Estimated effects (mm/year ± SE)	P-value
Ki-67	Complete	36	2.2	0.2±0.3	0.40
	Missing data	20	1.9		
Mutant p53	Complete	30	2.4	0.5±0.3	0.10
	Missing data	26	2		
TERT promoter	Complete	45	2.3	0.8±0.3	0.02*
	Missing data	11	1.5		
1p/19q	Complete	40	3.4	-0.14±0.4	0.68
	Missing data	16	2.2		
EGFR	Complete	16	3.2	1.4±0.3	<0.01*
	Missing data	40	1.8		
ATRX	Complete	25	2.3	0.3±0.3	0.26
	Missing data	31	1.9		
MGMT promoter	Complete	39	2.1	0.5±0.3	0.10
	Missing data	17	1.7		

*, A P-value ≤0.05 was considered statistically significant. VDE, velocity of diameter expansion; SE, standard error.

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Table S3 The estimated effect of multiple-factor analysis using the mLMEM in the diffuse astrocytoma, *IDH* mutant subgroup

Molecular biomarker	Estimated effects (mm/year ± SE)	P-value
Age	-0.09±0.03	0.01*
Mutant p53 (High *vs.* low expression)	3.6±1.7	0.04*
MGMT promoter (Methylation *vs.* non-methylation)	-2.6±0.5	< 0.01*

*, A P-value ≤0.05 was considered statistically significant. mLMEM, multivariate linear mixed-effects model; SE, standard error

Table S4 The estimated effect of multiple-factor analysis using the mLMEM in the oligodendroglioma, *IDH* mutant subgroup

Molecular biomarkers	Estimated effects (mm/year ± SE)	P-value
Age	-0.02±0.006	<0.01*
Gender (Female *vs.* male)	0.7±0.2	<0.01*

*, A P-value ≤0.05 was considered statistically significant. mLMEM, multivariate linear mixed-effects model; SE, standard error.

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